



#9

SEQUENCE LISTING

<110> Barber, Elizabeth K

<120> Gene Expression Control Element DNA

<130> 896034605001

<140> US 09/966,264

<141> 2001-09-28

<150> US 60/237,079

<151> 2000-09-30

<160> 61

<170> PatentIn version 3.1

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tga act cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga 95
Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys
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taa gta atc aatcaa tca ctc ata gcc aag gtg gaa aag atg tat ccc 96
Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro
20 25 30

atc atg gaa tat tcc tgt tct gat aga aat ctt gtg ctt atc tat gga 144
Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly
35 40 45

att ctt ttg ata tat att tac att ggg aac ctg aat gta gct tga cat 192

Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala His
50 55 60

ttt tcc atg taa aca cca gta gcc tga tcc aac att aag ctg ata cta 240
Phe Ser Met Thr Pro Val Ala Ser Asn Ile Lys Leu Ile Leu
65 70 75

aca aac aac gtg taa tgg ctt cat taa taa ggc ttt gct tct tcc tgg 288
Thr Asn Asn Val Trp Leu His Gly Phe Ala Ser Ser Trp
80 85

aaa ctg gtg aaa aat caa acc ttg ttg tgt aca ccc tcg atg cag ctt 336
Lys Leu Val Lys Asn Gln Thr Leu Leu Cys Thr Pro Ser Met Gln Leu
90 95 100

ctg tgt tgt ctt cac cca gaa atg ggg aat gat ttc cca aat ggc aaa 384
Leu Cys Cys Leu His Pro Glu Met Gly Asn Asp Phe Pro Asn Gly Lys
105 110 115 120

gaa aca gag tga tgc tat cta tct gca cct ttt gta aag tct gtc ttt 432
Glu Thr Glu Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe
125 130 135

ctt tct ctt tgt ttt cca gga cac aat gta gga agt ctt ttc cac atg 480
Leu Ser Leu Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met
140 145 150

gca gat gat ttg ggc aga gcg atg gag tcc tta gta tca gtc atg aca 528
Ala Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr
155 160 165

gat gaa gaa gga gca gaa taa atg ttt tac aac tcc tga ttc ccg cat 576
Asp Glu Glu Gly Ala Glu Met Phe Tyr Asn Ser Phe Pro His
170 175 180

ggt ttt tat aat att cat aca aca aag agg att aga cag taa gag ttt 624
Gly Phe Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln Glu Phe
185 190 195

aca aga aat aaa tct ata ttt ttg tga agg gta gtg gta tta tac tgt 672
Thr Arg Asn Lys Ser Ile Phe Leu Arg Val Val Val Leu Tyr Cys
200 205 210

aga ttt cag tag ttt cta agt ctg tta ttg ttt tgt taa caa tgg cag 720
Arg Phe Gln Phe Leu Ser Leu Leu Phe Cys Gln Trp Gln
215 220 225

gtt tta cac gtc tat gca att gta caa aaa agt tat aag aaa act aca 768
Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr
230 235 240

tgt aaa atc ttg ata gct aaa taa ctt gcc att tct tta tat gga acg 816
Cys Lys Ile Leu Ile Ala Lys Leu Ala Ile Ser Leu Tyr Gly Thr
245 250 255

cat ttt ggg ttg ttt aaa aat tta taa cag tta taa aga aag aat tat 864
His Phe Gly Leu Phe Lys Asn Leu Gln Leu Arg Lys Asn Tyr

260

265

270

aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act 912
Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu Thr
275 280

cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga 960
Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys Gly Arg
285 290 295

aat agc atg aga agc cgt gtt tga tgt taa tta att 996
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Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr Asp
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Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Met Lys Lys Glu Gln Asn Lys
35 40 45
Cys Phe Thr Thr Pro Asp Ser Arg Met Val Phe Ile Ile Phe Ile Gln
50 55 60
Gln Arg Gly Leu Asp Ser Lys Ser Leu Gln Glu Ile Asn Leu Tyr Phe
65 70 75 80
Cys Glu Gly Phe Tyr Thr Ser Met Gln Leu Tyr Lys Lys Val Ile Arg
85 90 95
Lys Leu His Lys Ile Thr Gln Trp Thr Arg Thr Pro Gln Asn Gln Ser
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Glu Val Glu Ile Ala
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35 40 45

Gly Asn Leu Asn Val Ala Arg His Phe Ser Met Lys Thr Pro Val Ala
50 55 60

Arg Ser Asn Ile Lys Leu Ile Leu Thr Asn Asn Val Lys Trp Leu His
65 70 75 80

Lys Lys Gly Phe Ala Ser Ser Trp Lys Leu Val Lys Asn Gln Thr Leu
85 90 95

Leu Cys Thr Pro Ser Met Gln Leu Leu Cys Cys Leu His Pro Glu Met
100 105 110

Gly Asn Asp Phe Pro Asn Gly Lys Glu Thr Glu Arg Cys Tyr Leu Ser
115 120 125

Ala Pro Phe Val Lys Ser Val Phe Leu Ser Leu Cys Phe Pro Gly His
130 135 140

Asn Val Gly Ser Leu Phe His Met Ala Asp Asp Leu Gly Arg Ala Met
145 150 155 160

Glu Ser Leu Val Ser Val Met Thr Asp Glu Glu Gly Ala Glu Lys Met
165 170 175

Phe Tyr Asn Ser Arg Phe Pro His Gly Phe Tyr Asn Ile His Thr Thr
180 185 190

Lys Arg Ile Arg Gln Lys Glu Phe Thr Arg Asn Lys Ser Ile Phe Leu
195 200 205

Arg Arg Val Val Val Leu Tyr Cys Arg Phe Gln Lys Phe Leu Ser Leu
210 215 220

Leu Leu Phe Cys Lys Gln Trp Gln Val Leu His Val Tyr Ala Ile Val
225 230 235 240

Gln Lys Ser Tyr Lys Lys Thr Thr Cys Lys Ile Leu Ile Ala Lys Lys
245 250 255

Leu Ala Ile Ser Leu Tyr Gly Thr His Phe Gly Leu Phe Lys Asn Leu
260 265 270

Lys Gln Leu Lys Arg Lys Asn Tyr Lys Gly Lys Arg Lys Lys Arg Asn
275 280 285

Gly Gln Val Val Lys Leu Arg Thr Gln Val Cys Thr Ile Ile Arg Asn
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Cys Lys Leu Ile

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att att att ttc aac cca agt aaa agc aga gag aaa ata gcc acc tcc 96
Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala Thr Ser
20 25 30

acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg aaa tga 144
Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu Lys
35 40 45

aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc gat ggt 192
Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr Asp Gly
50 55 60

tgg gtg ctg gtg atg gta gtg gta gtt gtg aag gtg gtg atg 234
Trp Val Leu Val Met Val Val Val Val Lys Val Val Met
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Gly Arg Asn Ser Met Arg Ser Arg Val
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Leu Ile Val Lys Lys Met Phe Val Asn Thr Ser Arg Glu
1 5 10

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Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro
1 5 10 15

Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr
20 25 30

Gly Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala
35 40 45

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Ser Asn Ile Lys Leu Ile Leu Thr Asn Asn Val
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<210> 41
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Gly Phe Ala Ser Ser Trp Lys Leu Val Lys Asn Gln Thr Leu Leu
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Cys Thr Pro Ser Met Gln Leu Leu Cys Cys Leu His Pro Glu Met
20 25 30

Gly Asn Asp Phe Pro Asn Gly Lys Glu Thr Glu
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Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe Leu Ser Leu
1 5 10 15

Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met Ala Asp
20 25 30

Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr Asp
35 40 45

Glu Glu Gly Ala Glu
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Glu Phe Thr Arg Asn Lys Ser Ile Phe Leu
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Arg Val Val Val Leu Tyr Cys Arg Phe Gln
1 5 10

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Phe Leu Ser Leu Leu Leu Phe Cys
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Gln Trp Gln Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr
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Lys Lys Thr Thr Cys Lys Ile Leu Ile Ala Lys
20 25

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Leu Ala Ile Ser Leu Tyr Gly Thr His Phe Gly Leu Phe Lys Asn Leu
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Arg Lys Asn Tyr Lys Gly Lys Arg Lys
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Phe Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala
-60 -55 -50

acc tcc acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg -96
Thr Ser Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu
-45 -40 -35

aaa tga aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc -48
Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr
-30 -25 -20

tgg gtg ctg gtg atg gta gtg gtt gtg aag gtg gtg atg gat ggt 0
Trp Val Leu Val Met Val Val Val Val Lys Val Val Met Asp Gly
-15 -10 -5

gtg gtt tga ttg ata gta aaa aaa atg ttc gtt aat aca agt aga gag 48

Val Val	Leu Ile Val Lys Lys Met Phe Val Asn Thr Ser Arg Glu	
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taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc	96	
Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro		
20	25	30
atc atg gaa tat tcc tgt tct gat aga aat ctt gtg ctt atc tat gga	144	
Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly		
35	40	45
att ctt ttg ata tat att tac att ggg aac ctg aat gta gct tga cat	192	
Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala His		
50	55	60
ttt tcc atg taa aca cca gta gcc tga tcc aac att aag ctg ata cta	240	
Phe Ser Met Thr Pro Val Ala Ser Asn Ile Lys Leu Ile Leu		
65	70	75
aca aac aac gtg taa tgg ctt cat taa taa ggc ttt gct tct tcc tgg	288	
Thr Asn Asn Val Trp Leu His Gly Phe Ala Ser Ser Trp		
80	85	
aaa ctg gtg aaa aat caa acc ttg ttg tgt aca ccc tcg atg cag ctt	336	
Lys Leu Val Lys Asn Gln Thr Leu Leu Cys Thr Pro Ser Met Gln Leu		
90	95	100
ctg tgt tgt ctt cac cca gaa atg ggg aat gat ttc cca aat ggc aaa	384	
Leu Cys Cys Leu His Pro Glu Met Gly Asn Asp Phe Pro Asn Gly Lys		
105	110	115
120		
gaa aca gag tga tgc tat cta tct gca cct ttt gta aag tct gtc ttt	432	
Glu Thr Glu Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe		
125	130	135
ctt tct ctt tgt ttt cca gga cac aat gta gga agt ctt ttc cac atg	480	
Leu Ser Leu Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met		
140	145	150
gca gat gat ttg ggc aga gcg atg gag tcc tta gta tca gtc atg aca	528	
Ala Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr		
155	160	165
gat gaa gaa gga gca gaa taa atg ttt tac aac tcc tga ttc ccg cat	576	
Asp Glu Glu Gly Ala Glu Met Phe Tyr Asn Ser Phe Pro His		
170	175	180
ggt ttt tat aat att cat aca aca aag agg att aga cag taa gag ttt	624	
Gly Phe Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln Glu Phe		
185	190	195
aca aga aat aaa tct ata ttt ttg tga agg gta gtg gta tta tac tgt	672	
Thr Arg Asn Lys Ser Ile Phe Leu Arg Val Val Val Leu Tyr Cys		
200	205	210
aga ttt cag tag ttt cta agt ctg tta ttg ttt tgt taa caa tgg cag	720	
Arg Phe Gln Phe Leu Ser Leu Leu Phe Cys Gln Trp Gln		

215

220

225

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Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr
230 235 240

tgt aaa atc ttg ata gct aaa taa ctt gcc att tct tta tat gga acg 816
Cys Lys Ile Leu Ile Ala Lys Leu Ala Ile Ser Leu Tyr Gly Thr
245 250 255

cat ttt ggg ttg ttt aaa aat tta taa cag tta taa aga aag aat tat 864
His Phe Gly Leu Phe Lys Asn Leu Gln Leu Arg Lys Asn Tyr
260 265 270

aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act 912
Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu Thr
275 280

cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga 960
Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys Gly Arg
285 290 295

aat agc atg aga agc cgt gtt tga tgt taa tta att 996
Asn Ser Met Arg Ser Arg Val Cys Leu Ile
300 305

<210> 52
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<400> 52

Phe Pro Ile Gln Cys Ile Val His Gln Arg Ser Ile Gln Glu Phe
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Thr Ser Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala
35 40 45

Leu Lys

<210> 53
<211> 32
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<213> human

<400> 53

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Gly Trp Val Leu Val Met Val Val Val Val Lys Val Val Met

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25

30

Val Val

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<212> DNA
<213> mouse

<400> 54

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ccaacaaagt gtgaaaggcg tgtgccatta cacatcttc tcggtgataa 200
gagccttgc tatgaagttc tgagatgtgt taggaagatg aatcatcaat 250
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tactaacacc atgcaatgct tcattaacaa ggatttgctt cttgctagaa 350
atgggttaaaa acggactgtg gtctgtatac cttcaatgca gcttatgtgt 400
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aataacttgc aactttgtaa actctttctt tctctttgtt ttccaggaca 500
caatgttagga agcctttcc acatggcaga tgatttggc agagcgatgg 550
agtccttagt ttcaagtcatg acagatgaag aaggagcaga ataaatgttt 600
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gattagacag taagagttt caagaaataa aatctatatt tttgtgaagg 700
gtatgtgtac tatactgttag atttcagtag tttctaagtc tgttattgtt 750
ttgttaacaa tggcagggtt tacacgtcta tgcaattgtt caaaaaagtt 800
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tatggAACGc attttgggtt gttaaaaat ttataacagt tataaagaaa 900
gattgtaaac taaagtgtgc tttataaaaa aagtgtttt taaaaacccc 950
taaacaaaca cacacgcaca cacacacaca cacacacaca cacacacaca 1000
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agttgggtgtg gcgggtatgg tggcagtgtat aatggtgacc gatggttggg 200
tgctggtgat ggttagtggta gttgtga.ag gtgggtatgg tggtttgatt 250
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<212> PRT
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<400> 56

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Leu Ile Tyr Gly Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu
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Asn Val Ala Arg His Phe Ser Met Lys Thr Pro Val Ala Arg Ser
35 40 45

Asn Ile Lys Leu Ile Leu Thr Asn Asn Val Lys Trp Leu His Lys
50 55 60

Lys Gly Phe Ala Ser Ser Trp Lys Leu Val Lys Asn Gln Thr Leu
65 70 75

Leu Cys Thr Pro Ser Met Gln Leu Leu Cys Cys Leu His Pro Glu
80 85 90

Met Gly Asn Asp Phe Pro Asn Gly Lys Glu Thr Glu Arg Cys Tyr
95 100 105

Leu Ser Ala Pro Phe Val Lys Ser Val Phe Leu Ser Leu Cys Phe
110 115 120

Pro Gly His Asn Val Gly Ser Leu Phe His Met Ala Asp Asp Leu
125 130 135

Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr Asp Glu Glu
140 145 150

Gly Ala Glu Lys Met Phe Tyr Asn Ser Arg Phe Pro His Gly Phe
155 160 165

Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln Lys Glu Phe Thr
170 175 180

Arg Asn Lys Ser Ile Phe Leu Arg Arg Val Val Val Leu Tyr Cys
185 190 195

Arg Phe Gln Lys Phe Leu Ser Leu Leu Phe Cys Lys Gln Trp
200 205 210

Gln Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys
215 220 225

Thr Thr Cys Lys Ile Leu Ile Ala Lys Lys Leu Ala Ile Ser Leu
230 235 240

Tyr Gly Thr His Phe Gly Leu Phe Lys Asn Leu Lys Gln Leu Lys
245 250 255

Arg Lys Asn Tyr Lys Gly Lys Arg Lys Lys Arg Asn Gly Gln Val

260

265

270

Val Lys Leu Arg Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro
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275

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285

Lys Pro Lys Arg Gly arg Asn Ser Met Arg Ser Arg Val Arg Cys
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Lys Leu Ile

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ATTGCGTTAT	TTTCTTTTC	CTTTATAATT	CTTTCTTTT	CCTTCATAAT	200	
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<212> PRT

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<400> 61

Met Tyr Pro Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val
1 5 10 15

Leu Ile Tyr Gly Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu
20 25 30

Asn Met Lys Lys Glu Gln Asn Lys Cys Phe Thr Thr Pro Asp Ser
35 40 45

Arg Met Val Phe Ile Ile Phe Ile Gln Gln Arg Gly Leu Asp Ser
50 55 60

Lys Ser Leu Gln Glu Ile Asn Leu Tyr Phe Cys Glu Gly Phe Tyr
65 70 75

Thr Ser Met Gln Leu Tyr Lys Lys Val Ile Arg Lys Leu His Lys
80 85 90

Ile Thr Gln Trp Thr Arg Thr Pro Gln Asn Gln Ser Glu Val Glu
95 100 105

Ile Ala